

GenCore version 5.1.4-p5-4578 Copyright (c) 1993 - 2003 Compugen Ltd.											
OM protein - protein search, using sw model											
Run on: April 8, 2003, 14:23:17 ; Search time 14 Seconds											
(without alignments)											
1614.614 Million cell updates/sec											
Title: US-09-001-737-8	perfect score: 2663	Sequence: 1 MAKEIKFSADARAAMYRGVD. .... .TPAPAMPAGMDPGMMGAGG 545									
Scoring table: Biosum62	Gapop 10.0	Gapext 0.5									
Searched: 112892 seqs, 41476328 residues	Total number of hits satisfying chosen parameters: 112892	Minimum DB seq length: 0	Maximum DB seq length: 200000000								
Post-processing: Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries									
Database: SwissProt_40;*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query Match Length	DB ID	Description	RESULT 1	CH60_STRPY	STANDARD;	PRT;	542 AA.		
1	2038	99.1	542	1 CH60_STRPY	CH60_STRPY	CH60_STRPY	PRT;	542 AA.			
2	2195.5	82.4	542	1 CH60_LACIA	P8485	STREPTOCOCCUS	PARTIAL SEQUENCE, AND MASS SPECTROMETRY.				
3	2033.5	76.4	542	1 CH60_LIMNO	P37282	LACTOCOCCUS	STRAIN-JRS4 / SEROTYPE M6;				
4	2026.5	76.1	539	1 CH60_BACST	Q96966	listeria mo	Q07201 bacillus st				
5	2026.5	76.1	542	1 CH60_LININ	Q95200	listeria in	P25998 bacillus su				
6	2021.5	75.9	543	1 CH60_BACSU	P25998	bacillus su	Q51305 bacillus ha				
7	2017.5	75.8	544	1 CH60_BACHD	P26209	bacillus ps	P26209 bacillus ps				
8	1881	74.4	538	1 CH60_BACP3	Q68324	lactobacilli	P49218 staphylococ				
9	1877.5	70.5	540	1 CH60_LAHE	Q08854	staphylococ	Q08854 staphylococ				
10	1857.5	69.8	538	1 CH60_STREP	P42112	clostridium	P42112 clostridium				
11	1842.5	69.2	538	1 CH60_STRAU	P26221	clostridium	P26221 clostridium				
12	1833.5	68.9	540	1 CH60_CLOTM	P30117	clostridium	P30117 clostridium				
13	1818	68.3	539	1 CH60_CLOPE	Q60024	thermoanaerobacter	Q60024 thermoanaer				
14	1776	66.7	543	1 CH60_CLOAB	P47146	thermus the	P47146 thermus the				
15	1723.5	64.7	540	1 CH60_THERB	P42118	mycobacteri	P42118 mycobacteri				
16	1706	64.1	542	1 CH60_THERH	P36468	leptospira	P36468 leptospira				
17	1697	63.7	540	1 CH60_MYCPA	P92849	rhizobium m	P92849 rhizobium m				
18	1688.5	63.4	546	1 CH60_LEIDIN	P35569	rhizobium m	P35569 rhizobium m				
19	1678.5	63.0	545	1 CH60_RHME	Q94622	paracoccus	Q94622 paracoccus				
20	1674.5	62.9	545	1 CH60_RHME	P25957	brucella ab	P25957 brucella ab				
21	1670.5	62.7	546	1 CH60_BRBR	Q93954	hemocyste	Q93954 hemocyste				
22	1670.5	62.5	538	1 CH60_BRBR	P30179	agrobacteri	P30179 agrobacteri				
23	1663.5	62.2	538	1 CH60_BRBR	P96139	rhizobium l	P96139 rhizobium l				
24	1661.5	62.4	544	1 CH60_BRBR	P20110	rhodobacter	P20110 rhodobacter				
25	1660	62.3	546	1 CH60_RHBL	P30118	rhodobacter	P30118 rhodobacter				
27	1657.5	62.2	545	1 CH61_BRSH	P97712	rhodobacter	P97712 rhodobacter				
28	1656	62.2	546	1 CH61_BRSH	P06118	rhodobacter	P06118 rhodobacter				
29	1654	62.1	544	1 CH60_NEKMA	P51006	neisseria m	P51006 neisseria m				
30	1653	547	1 CH60_SALTY	P48217	salmonella m	P48217 salmonella m					
31	1651	62.0	547	1 CH60_BAQU	Q97712	bartholomaei	Q97712 bartholomaei				
32	1646	61.8	539	1 CH62_STRAU	P06139	streptomyce	P06139 streptomyce				
33	1646	61.8	546	1 CH60_BURPS	P97712	burkholderia	P97712 burkholderia				

SQ	SEQUENCE	542 AA:	56964 MW;	C759A139B6FD71D4 CRC64;	RT	lactis ssp. <i>lactis</i> IT1403 *
Query Match						
Best Local Similarity	99.1%	Score	2638;	DB 1;	Length	542;
Matches	540;	Pred.	No.	1.6e-14;		
Conservative	1;	Mismatches	0;	Indels	0;	Gaps
OY	2	AKIIFKSDARAMTRGVMADTVKTVLGPCKRNVLKAFESPLTNDGCVTAKETE	61	CC	-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS	
Db	1	AKIIFKSDARAMTRGVMADTVKTVLGPCKRNVLKAFESPLTNDGCVTAKETE	60	CC	-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).	
OY	122	ATRVEALKALQPVSKRVEAVVASSERKVEYISAMERVENDGTVTEESMG	181	CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.	
Db	121	ATRVEALKALQPVSKRVEAVVASSERKVEYISAMERVENDGTVTEESMG	180	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
OY	182	ETELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	241	CC	DR: EMBL: X71132; CAA50446; 1; -.	
Db	161	ETELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	240	CC	DR: EMBL: AB005276; AAC04492; 1; -.	
OY	242	NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	301	CC	DR: PIR: S22100; S32106.	
Db	241	NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	300	CC	DR: PIR: S22101; S32105.	
OY	302	DGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	361	CC	DR: PRINTS: PRO0304; TCOMPLEXCF.	
Db	301	DGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	360	CC	DR: PROSITE: PS00096; CHAPERONINS_CNC60; 1.	
OY	362	KLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	421	CC	DR: Chaperone; ATP-binding; Complete proteome.	
Db	361	KLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	420	CC	DR: FT: CONFLICT: 89 T -> N (IN REF.);	
OY	422	EVKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	481	CC	DR: FT: CONFLICT: 289 D -> H (IN REF.);	
Db	421	EVKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	480	CC	DR: FT: CONFLICT: 367 L -> V (IN REF.);	
OY	482	WMDWIKIGIDPPVTRALQNAVASILITTEAVVANKPEPATPAPMAGDPMG	541	CC	DR: FT: CONFLICT: 542 M -> I (IN REF.);	
Db	481	WMDWIKIGIDPPVTRALQNAVASILITTEAVVANKPEPATPAPMAGDPMG	540	CC	DR: SQ: SEQUENCE: 542 AA: 57201 MW: D7D6F5319DA59721 CRC64;	
Query Match						
Best Local Similarity	81.1%	Score	2195.5;	DB 1;	Length	542;
Matches	442;	Pred.	No.	3.2e-94;		
Conservative	52;	Mismatches	46;	Indels	5;	Gaps
OY	1	MAKEIKSDARAMTRGVMADTVKTVLGPCKRNVLKAFESPLTNDGCVTAKETE	60	CC	Db: 1 WSKDKFKESSDARTAMTRGVMADTVKTVLGPCKRNVLKAFESPLTNDGCVTAKETE 60	
Db	121	LAETEVAVASIKENIATVHRSKATQAVTVASSERKVEYISAMERVENDGTVTEESMG	180	CC	Db: 121 LAETEVAVASIKENIATVHRSKATQAVTVASSERKVEYISAMERVENDGTVTEESMG	
OY	181	METELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	240	CC	Db: 181 METELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	
Db	181	METELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	240	CC	Db: 181 METELEVYGMOPDRYLSQYMTDNKMKMADLENPLITDKVSNIQDPLILEEVK	
OY	241	NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	300	CC	Db: 241 NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	
Db	241	NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	300	CC	Db: 241 NRPLIILADDGEALPPTVILKIRGTVENVAKPGFGRKAMILEDIALTGTIVTE	
OY	301	EDGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	360	CC	Db: 301 EDGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	
Db	301	EDGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	360	CC	Db: 301 EDGIEKIKATMVALQQAQKITYDKSTVIVVEGSEATANRALKSISQETTSDFDR	
OY	361	ERLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	420	CC	Db: 361 ERLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	
Db	361	ERLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	420	CC	Db: 361 ERLQLRLAKLAKLAGGVAVIKVKGAPTEALKERKTREDALNTRAAVEEVGGTALIV	
OY	421	TEKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	480	CC	Db: 421 TEKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	
Db	421	TEKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	480	CC	Db: 421 TEKVALELEGDAATGRNIVRLAEPVROIAJANGEGSVIQLKNSPAGTGFNAATGE	
OY	481	WMDWIKIGIDPPVTRALQNAVASILITTEAVVANKPEPATPAPMAGDPMG	540	CC	Db: 481 WMDWIKIGIDPPVTRALQNAVASILITTEAVVANKPEPATPAPMAGDPMG	

RT: MEDLINE:9332268; PubMed=8486277;

RA: Kim S.G., Batt C.A.;

RT: "Cloning and sequencing of the *Lactococcus lactis* subsp. *lactis*

RT: *groEL* operon",

RL: Gene 17:121-126 (1993).

[2] SEQUENCE FROM N.A.

RC: STRAIN=IL103;

RX: MEDLINE:2135186; PubMed=11337471;

RA: Böltin A., Wincker P., Mauger S., Jallion O., Malarme K.,

RA: Weissbach J., Enlich S.D., Sorokin A.;

RT: "The complete genome sequence of the lactic acid bacterium *Lactococcus*











Matches 363; Conservative 87; Mismatches 88; Indels 1; Gaps 1;

QY 241 TNPFLIITADDVPGEAUPTVLNKIRGTEVNVAVKAPCGFCDRKAMEDIAILLAGTGTIVT 300  
 DB 241 QGKSLIADDITGEAULPTVLNKIRGTFNVAKAFCFGDFDRRAQDIAUTGTTVIT 300  
 QY 301 EDEGJELKQATMPLGQAKITDQSTTVEGSGSEANRITALKSOLETTSDDR 360  
 DB 301 EDEGJELKQATMPLGQAKITDQSTTVEGSGSEANRITALKSOLETTSDDR 360  
 QY 361 EKQERLAKLAGVAVIKGAPPTALKENKLRTEDALNATRAAWEVREGVAGGTALITY 420  
 DB 361 KKLQERLAKLAGVAVIKGAPPTALKENKLRTEDALNATRAAWEVREGVAGGTALITY 420  
 QY 421 IEKVALELEG --DQATGRNIVALEEVROTALNAGVEGSVWIDKLKNSPAGTGENA 477  
 DB 421 IEKVALELEG --DQATGRNIVALEEVROTALNAGVEGSVWIDKLKNSPAGTGENA 477  
 QY 478 ATGENDVMIKTTGIDVVKVRSALQNAVASLILTEAVWANKREPATPAPMGPMDP 537  
 DB 479 ATDKNENWVDAQGIDPTKVTRALQNAVASLILTEAVWAEPEPKQAPQGAGAPM 538  
 QY 538 GM 539  
 DB 539 GM 540

RESULT 10

CH60\_STAEV ID: C860\_STAEV STANDARD: PRT; 538 AA.  
 AC P8213; DT 01-FEB-1998 (Rel. 33, Created)  
 CC 01-FEB-1998 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60, kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein  
 DE 60),  
 GN GROEL OR MOPA OR HSP60.  
 OS Staphylococcus epidermidis.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TAXID-1282;  
 RN [1]  
 RP SEQUENCE FROM N.A.,  
 RC STRAIN#9759;

RA Gon S.H., Wood J., Hemmingsen S., Chow A.W.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announces/>  
 CC EMBL; U1618; AAC21334.1; -.  
 DR HSP60; P06139; IGRL.  
 DR InterPro; IPR002423; Chaperonin\_Cpn60.  
 DR Pfam; PF00118; Cpn60\_TCP\_1.  
 DR PRINTS; PRO009; CHAPERONIN\_0.  
 DR PROSITE; PS00296; CHAPERONIN\_CPN60\_1.  
 DR Chaperone; ATP-Binding; Heat shock protein; HSP60; IGRL.  
 FT INTR-MET 0 0 BY SIMILARITY.  
 SO SEQUENCE 538 AA; 5718 MW; 8DARE9A6246C8E6 CRC64;

Query Match 69.8%; Score 1857.5; DB 1; Length 538;  
 Best Local Similarity 67.3%; Pred. No. 1e-78;

Matches 363; Conservative 87; Mismatches 88; Indels 1; Gaps 1;

QY 2 AKEIKFSDARAAMYRGMDADTVKVLGPGKGRNVLKAFGSPPLITDGVMIAKIEL 61  
 DB 1 AKDKEFSDARQAMLRGQDULANAVKVTGPKGRNVLKDFDITPLITNGVIAKIEL 60  
 QY 62 EDHFENNGAKLYVEASVNSTNDIAGSGTTATVLTIAVHEGKNTVAGANPPIGRIGIET 121  
 CC 61 EDHYENNGAKLYVEASVNSTNDIAGSGTTATVLTIAVHEGKNTVAGANPPIGRIGIET 121  
 DB 122 ATRAVELAKRAOPVSKREAQAVAVSRSERKVEYTSSEMERVGNDGVITIERSRM 181  
 QY 121 AVOVATEALHEISOKVENKNEIAQVGAISADEEIGRYISEANDKVNGDGVITIERSNG 180  
 DB 182 ETLEVEVKGKLUQVQVANKTNEIAGDTTATVLAQSMOEGLKNTVSGANPPVLRQIDK 241  
 DB 181 NTLEVAKRQVSKREAQAVAVSRSERKVEYTSSEMERVGNDGVITIERSRM 181  
 QY 242 NRFLIITADDVYDGEALTVLNUKTRGTEVNVAVKPGFDRKAMEDIAILJGCVITE 301  
 DB 241 SRFLIVADVEGDLANLNUKTRGTEVNVAVKPGFDRKAMEDIAILJGCVITE 300  
 QY 302 DUGLEERDANTALGQAKITVVDQSTVIEGSGSEANITALKSOLETTSDPDR 361  
 DB 301 DUGLEERDANTALGQAKITVVDQSTVIEGSGSEANITALKSOLETTSDPDR 361  
 QY 362 KQERLAKLAGVAVIKGAPPTALKENKLRTEDALNATRAAWEVREGVAGGTALITY 421  
 DB 361 KQERLAKLAGVAVIKGAPPTALKENKLRTEDALNATRAAWEVREGVAGGTALITY 420  
 QY 422 EKVALELEGDDATGRNIVALEEVROTALNAGVEGSVWIDKLKNSPAGTGENA 481  
 DB 421 QVSEIRKAEGDVEGTVGVNVIKALQAPQIENAGLEGSIIVERLKHAEAGVGPNAIE 480  
 QY 482 WMDMVKIGIDPTKVRSALQNAVASLILTEAVWANKREPATPAPMGPMDPMM 540  
 DB 481 WMDMVKIGIDPTKVRSALQNAVASLILTEAVWANKREPATPAPMGPMDPMM 538

RESULT 11

CH60\_STAAU ID: C160\_STAAU STANDARD: PRT; 538 AA.  
 AC P08854; DT 01-OCT-1994 (Rel. 30, Created)  
 CC 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein  
 DE 60),  
 GN GROEL OR MOPA OR HSP60.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TAXID-1280;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN#912;  
 RX MEDLINE-91290569; PubMed-7916607;  
 RA Ohta T., Honda K., Kuroda M., Saito K., Hayashi H.;  
 RT "Molecular characterization of the gene operon of heat shock proteins  
 RL HSP60 and HSP10 in methicillin-resistant Staphylococcus aureus.";  
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic.  
 CC -1- INDUCTION BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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QY	362	KIQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI	421	KW	Chaperone: ATP-binding; Complete proteome.
DR	361	KIQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI	420	FT	CONFICT 344
QY	422	TERVALA--FLEDDATGRNVLRALEPVRQVIAVNLNAGYEGSVVYDVKNSPACTGPNRAT	479	PT	344
DR	421	TERVALA--FLEDDATGRNVLRALEPVRQVIAVNLNAGYEGSVVYDVKNSPACTGPNRAT	479	SEQUENCE	344
QY	480	GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPAPAPMPGMPGM	539	Q9Y	1 MAKEIKFSADARAMYVGCVOMLADTVKTLGPKGNVNLKAFGSPPLITNDCYTKE 60
DR	481	GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPAPAPMPGMPGM	539	DR	1 MARTLLEGEBAKRSMQGVKLAKVTKLPGPKGNVNLKFGSPPLITNDGYTKE 60
QY	540	MGGM	539	Q9Y	61 LEDEHFNMGAKLSEVAKNDTAGDGTITATVJTOAIVHCKVNTAGANPIGIRGIE 120
DR	536	MGGM	539	DR	61 LEDEHFNMGAKLSEVAKNDTAGDGTITATVJTOAIVHCKVNTAGANPIGIRGIE 120
RESULT 13					
ID	CH60_CLOPE	STANDARD:	PRT:	QY	121 TATATATVAKATAQPVSGEIAQVAVASSERSEVGVYTBAMRVGFDGTYTESRG 180
AC	P68211;			DR	121 TATATATVAKATAQPVSGEIAQVAVASSERSEVGVYTBAMRVGFDGTYTESRG 180
DT	01-AUG-1992 (Rel. 23, Created)			QY	161 METELLEVMEQMDRGLSOMVTDNEWMWDLNEMPLDILDKVSNQDIPLBEVK 240
DT	15-JUN-2002 (Rel. 41, Last sequence update)			DR	161 METELLEVMEQMDRGLSOMVTDNEWMWDLNEMPLDILDKVSNQDIPLBEVK 240
DE	60 kDa chaperonin (Protein Cpn60) (groEL protein).			QY	181 METELLEVMEQMDRGLSOMVTDNEWMWDLNEMPLDILDKVSNQDIPLBEVK 240
GN	GROEL OR MOPA OR GROEL OR Cpn60.			DR	181 METELLEVMEQMDRGLSOMVTDNEWMWDLNEMPLDILDKVSNQDIPLBEVK 240
OS	Clostridium perfringens			QY	241 TNRPLIADDVGAEALPTVLNKKIRGTFNNVAKAPGFGRRKAMLDIAITLGTVT 300
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			DR	241 TNRPLIADDVGAEALPTVLNKKIRGTFNNVAKAPGFGRRKAMLDIAITLGTVT 300
OX	Clostridium.			QY	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
NEBI_TAXID=1502;				DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RN	[1]			QY	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RP	SEQUENCE FROM N.A.			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RP	MEDLINE=2183020;			QY	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RA	PUBMED=11793842;			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RA	Rusanganya E., Singh B., Gupta R.S.;			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RT	Cloning of HSP60 (groEL) operon from <i>Clostridium perfringens</i> using a			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RT	polymerase chain reaction based approach.;			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RL	Biochim. Biophys. Acta 1130:90-94 (1992).			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
RT	[2]			DR	361 EKQLERLAKLAGSVAVYKVGAPTTALKEMKRLTDEDALNARAYEVGIVAGGGALITYI
CC	SEQUENCE FROM N.A.			QY	421 INEVAKNLDIDGEDEQVNGINNIVSLESPMQLAHNAGLEGVIEVVKNSDAGVSDAII
CC	SPRATN-13 / TYPE A;			DR	421 INEVAKNLDIDGEDEQVNGINNIVSLESPMQLAHNAGLEGVIEVVKNSDAGVSDAII
CC	SPRATN-13 / TYPE B;			QY	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE C;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE D;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE E;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE F;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE G;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE H;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE I;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE J;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE L;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE M;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE N;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE O;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE P;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE R;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE T;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE U;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE V;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE W;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE CC;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE DD;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE EE;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE II;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE QQ;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE XX;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE BB;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE NN;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE OO;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE YY;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE ZZ;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE CC;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE DD;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE EE;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE FF;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE GG;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE HH;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE II;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE JJ;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE KK;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE LL;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE QQ;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE BB;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE CC;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE HH;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE II;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
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CC	SPRATN-13 / TYPE KK;			DR	420 GRVDMIKIGIDPVKVTSLONASVAVLILTEAVANKPEPPATPAPAPMDP
CC	SPRATN-13 / TYPE LL;				

RX MEDLINE-21339325; PubMed-11466286;  
 RA Neelling J.; Breton G.; Omelchenko M.V.; Makarova K.S.; Zeng Q.;  
 RA Gibson R.; Lee H.M.; Dubois J.; Olu D.; Hitti J.; Wolf Y.J.;  
 RA Tatusov R.L.; Sabathe F.; Doucette-Stamm L.; Soucalle P.; Daly M.J.;  
 RA Bennett G.N.; Koonin E.V.; Smith D.R.;  
 RT Genome sequence and comparative analysis of the solvent-producing  
 bacterium *Clostridium acetobutylicum*;  
 RL J. Bacteriol. 183:4823-4838(2001).  
 CC -I. FUNCTION: PREVENTS ISFOLDING AND PROMOTES THE REFOLDING AND  
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC -I. SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC -I. SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 CC  
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 CC  
 DR EMBL: M74572; AAA3243\_1;  
 DR EMBL: AE00776; ARK80649\_1; -.  
 DR PIR: BA1877; BA1872.  
 DR HSSP: P06119; IGRL.  
 DR InterPro: IPR001844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60\_TCP-1.  
 DR Pfam: PF00117; CPN60\_TCP; 1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PRINTS: PR00304; TCOMPLEXTCPL.  
 DR PROSITE: PS00096; CHAPERONINS\_CPN60; 1.  
 KW CHaperone; ATP-binding; complete proteome.  
 SQ SEQUENCE 543 AA; 58073 MW; 6FD16C2E9DA03DAC CRC64;  
  
 Query Match 66.7%; Score 1776; DB 1; Length 543;  
 Matches 362; Conservative 78; Mismatches 100; Indels 6; Gaps 4;  
 QY 1 MAKEIKFSADARAMYGVYDNLADTVKTYLPGPKGRNVYLEKAFGSPPLITNDGVTAKIEIE 60  
 Db 1 MAKQIYLGGEARAKQYQKEYATKNDYAGDGTATTLAQAIIRGKQVNTAGANPMLNRG 120  
 QY 61 LEDHEFMKAQYKUSEQSKNDAGDGTATVQATVHECKVATGANGIIRGIE 120  
 Db 61 LEDPENKMGKQYQKEYATKNDYAGDGTATTLAQAIIRGKQVNTAGANPMLNRG 120  
 QY 121 TATATAVEELAKAOPVSGKEAQAVAVSRSRKEVGYIISSEAMERYGNDGVTTEESKG 180  
 Db 121 LAVDKTVEGEKKVSKVNGKEDARVASIRADPEIGKLIADAMKVGEGYITVTEESKG 180  
 QY 181 METELEVGVGMOPDRGYSQMYTDNEKMPADLENPFLITDKVSNIDOLPPLBEVK 240  
 Db 181 MCTELDVYGMQFDRYLSYMTQEMXMEAVLDPPLITDKKIANIQEILPPLQIVQ 240  
 QY 241 TNRPLLIIDDDGEALPLTVLNRGTFENNAVAKPQFGQRKAMSDIATLSTGTVT 300  
 Db 241 OCKKLIIDDDGEALPLTVLNRGTFENNAVAKPQFGQRKAMSDIATLSTGTVT 300  
 Db 241 EDLGLKQRTMQLQOAKITVQDSTVWEGGSSEAIANALIKSQLTTTSDFDR 360  
 QY 301 TNRPLLIIDDDGEALPLTVLNRGTFENNAVAKPQFGQRKAMSDIATLSTGTVT 300  
 Db 301 SELGKDKVQYKVEDLQSAEVSQKISKENTTINGHGDQSAIHDRVQIOTETTSDFDR 360  
 QY 361 EKQPLRLAKLAGVAVKQGAPTEKMKLREDALNTRAAVEEVVGGGAG 420  
 Db 361 EKQPLRLAKLAGVAVKQGAPTEKMKLREDALNTRAAVEEVVGGGAG 420  
 QY 421 TEKVALEL-EQDDATGGRVNLVALEPVGQIAINACYEGVYDVKLNNSPAGTGFNAAT 479  
 Db 421 LEPEVRLISLDEPDVQGINIVKALEPVGQIANNAGLEGSVIIEKINSEKGICFDAH 480  
 QY 480 GEWVDMIKYIIPVVKVTRSLONAASVASILTEAVVANKPEPATPAPNPGMDPCM 539

Db 481 EKVNDMLSGIVNDPTKVRSLONAASVASTFLTEAVADIPF--KDKPMPGGA-GGM 537  
 DR 540 MGGMG 545  
 QY 540 MGGMG 545  
 Db 538 --GMG 541

RESULT 15  
 CH60-TBRR ID: CH60\_TBRR STANDARD: PRT; 540 AA.  
 AC 060024;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).  
 GN GROEL OR MORA OR GROEL.  
 OS Thermomanaerobacter brockii (Thermomanaerobium brockii).  
 OC Bacteria; Firmicutes; Clostridia; Thermomanaerobacteriaceae; Thermomanaerobacter.  
 OX NCBI\_TaxID:29323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RT8\_G4;  
 RX MEDLINE-99014233; Pubmed-9795109;  
 RA Truscott K.N.; Scopes R.K.;  
 RT "Sequence analysis and heterologous expression of the groE genes from  
 RT Thermomanaerobacter sp. RT8\_G4.";  
 RL Gene 217:15-23 (1998).  
 RN [2]  
 RP SEQUENCE OF 1-43, AND CHARACTERIZATION  
 RC STRAIN=RT8\_G4;  
 RX MEDLINE-94291621; Pubmed-7912671;  
 RA Truscott K.N.; Hoej P.B.; Scopes R.K.;  
 RT "Purification and characterization of chaperonin 60 and chaperonin 10  
 RT from the anaerobic thermophile Thermomanaerobacter brockii.";  
 RL Eur. J. Biochem. 222:277-284 (1994).  
 CC -I. FUNCTION: PREVENTS ISFOLDING AND PROMOTES THE REFOLDING AND  
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC -I. CONDITIONS: BY SIMILARITY.  
 CC -I. 7 SUBUNITS (BY SIMILARITY).  
 CC -I. MASS SPECTROMETRY: MW=57949; MR=ERR-10; METHOD=Electrospray.  
 CC -I. SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 CC  
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 CC  
 DR U56021; ARB00559\_1; -.  
 DR HSSP; P01319; IGRL.  
 DR InterPro: IPR001844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60\_TCP-1.  
 DR PRINTS: PR00298; CHAPERONIN60.  
 DR PRINTS: PR00304; TCOMPLEXTCPL.  
 DR PROSITE: PS00096; CHAPERONINS\_CPN60; 1.  
 KW Chaperone; ATP-binding.  
 FT INIT-MET: 0  
 FT CONFLICT: 0  
 SQ SEQUENCE 540 AA; 57928 MW; 27C316D35C61734 CRC64;  
  
 Query Match 64.7%; Score 1723; DB 1; Length 540;  
 Best Local Similarity 64.9%; Pred. No. 1.4e-72;  
 Matches 349; Conservative 80; Mismatches 106; Indels 3; Gaps 2;  
 QY 2 AKEIKFSADARAMYGVYDNLADTVKTYLPGPKGRNVYLEKAFGSPPLITNDGVTAKIEIE 61  
 Db 1 AKQKQYGEARAKLAGVAVKQGAPTEKMKLREDALNTRAAVEEVVGGGAG 60

QY 62 EDHFSMNGAKLUSVASKNDIAGDGTTRATVJQAHGKNTAGAHPIGRIGET 121  
 ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 61 EDPFNGQGQKLEAKTKNDIAGDGTTRTQAQNVREGKLNLANGANPMLRSGIAK 120  
 QY 122 ATATAVEALKATAQPVSGEALQAVAVSSEKSGYTSAMERVENDGVTIBERGM 181  
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 Db 121 AVDAVEGKURSKPDKNESTAHAVISIADEECKLIAEMDKVODVITEECKT 180  
 QY 182 ETELEVVGOMDGRGLSOMTNDNERMADLENPTPLTIDKAVSNQDILPLBEEVLT 241  
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 Db 181 OTTLEUVVGMDPDRYISPYMVTAKMVERVLEPVYLIDKIKNTODLPLBEOVQO 240  
 QY 242 NRPLITADYDVGGEALPTLVLUKIRCTENMVAVKAGFGRKAMMEDIALLIGGYITE 301  
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 Db 241 CRKKLJLIAIDVYGEALATUVKRGTCVAKAGFCDRKEMQDIALTGGOVSE 300  
 QY 302 DUGLEBKATMVALQOAKITDKOSTVUVEGSSSEANRALKSQLETTSDPDR 361  
 ;||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 301 ELGDLKVRMLMGRAROKVTKERTTIVGGDPESEIKRKYNOIKAQIEETSDIDRE 360  
 QY 362 KLORLAKLAKGAVYTKVAPETALKENKLRTEDALNTRAAVEGIVGGTALITVI 421  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 361 KLORLAKLAKGAVYTKVAPETALKENKLRTEDALNTRAAVEGIVGGTALITVI 420  
 QY 422 ERVVAL - ELEGDTATGNIVRALKALEEPYRQATLNAHGYSVVIDLKNNS - PAGTGNAA 478  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 421 EDVOKVVDLSDGDFITGAKIVRALKALEEPYRQATLNAHGYSVVIDLKNNS - PAGTGNAA 480  
 QY 479 TGERVYDMITKGIGIDPKVTRSLQNAVASILTEAVANKPEPATPAPAMPAGND 536  
 |:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 481 KEEFTDMFKAGIVDPTKVTRALONASIASMLTTEAVDIPENKTGKPNPGAGND 538

Search completed: April 16, 2003, 14:23:41

Job time : 16 secs